

SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION:
- (i) APPLICANT: Papathanassiu, Adonia E
Green, Shawn J.
- 10 (ii) TITLE OF INVENTION: Compositions and Methods for
Inhibiting Cellular Proliferation
- (iii) NUMBER OF SEQUENCES: 2
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Jones & Askew
(B) STREET: 191 Peachtree Street, 37th Floor
(C) CITY: Atlanta
(D) STATE: Georgia
20 (E) COUNTRY: U.S.A.
(F) ZIP: 30303
- (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Greene, Jamie L.
(B) REGISTRATION NUMBER: 32,467
(C) REFERENCE/DOCKET NUMBER: 05213-0290
- (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (404) 818-3700
(B) TELEFAX: (404) 818-3799

(2) INFORMATION FOR SEQ ID NO:1:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- 20 (ix) FEATURE:
 (A) NAME/KEY: Active-site
 (B) LOCATION: 2..3
 (D) OTHER INFORMATION: /note= "Site of partial
25 phosphorylation"
- (ix) FEATURE:
 (A) NAME/KEY: Active-site
 (B) LOCATION: 117..118
30 (D) OTHER INFORMATION: /note= "Potential site for N-linked
glycosylation"
- (ix) FEATURE:
 (A) NAME/KEY: Active-site
35 (B) LOCATION: 167..168
 (D) OTHER INFORMATION: /note= "Potential site for N-linked
glycosylation"
- (ix) FEATURE:
40 (A) NAME/KEY: Active-site
 (B) LOCATION: 228..229
 (D) OTHER INFORMATION: /note= "Potential site for N-linked
glycosylation"
- 45 (ix) FEATURE:
 (A) NAME/KEY: Domain
 (B) LOCATION: 26..76
 (D) OTHER INFORMATION: /label= Kunitz-1

(ix) FEATURE:

(A) NAME/KEY: Domain

(B) LOCATION: 97..147

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(D) OTHER INFORMATION: /label= Kunitz-2

(ix) FEATURE:

(A) NAME/KEY: Domain

(B) LOCATION: 189..239

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(D) OTHER INFORMATION: /label= Kunitz-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu
 1 5 10 15

Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp
 20 25 30

20

Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr
 35 40 45

25

Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn
 50 55 60

Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn
 65 70 75 80

30

Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe
 85 90 95

Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg
 100 105 110

35

Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly
 115 120 125

40

Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys
 130 135 140

Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly
 145 150 155 160

45

Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys
 165 170 175

Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro
 180 185

Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn
 195 200 205
 5 Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly
 210 215 220
 Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys
 225 230 235 240
 10 Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys
 245 250 255
 Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe
 15 260 265 270
 Val Lys Asn Met
 275

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
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 (ii) MOLECULE TYPE: protein
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 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 40
 (v) FRAGMENT TYPE: N-terminal
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5	Asp	Ala	Ala	Gln	Glu	Pro	Thr	Gly	Asn	Asn	Ala	Glu	Ile	Cys	Leu	Leu	1	5	10	15
	Pro	Leu	Asp	Tyr	Gly	Pro	Cys	Arg	Ala	Leu	Leu	Leu	Arg	Tyr	Tyr	Tyr	20	25	30	
10	Asp	Arg	Tyr	Thr	Gln	Ser	Cys	Arg	Gln	Phe	Leu	Tyr	Gly	Gly	Cys	Glu	35	40	45	
	Gly	Asn	Ala	Asn	Asn	Phe	Tyr	Thr	Trp	Glu	Ala	Cys	Asp	Asp	Ala	Cys	50	55	60	
15	Trp	Arg	Ile	Glu	Lys	Val	Pro	Lys	Val	Cys	Arg	Leu	Gln	Val	Ser	Val	65	70	75	80
	Asp	Asp	Gln	Cys	Glu	Gly	Ser	Thr	Glu	Lys	Tyr	Phe	Phe	Asn	Leu	Ser	85	90	95	
20	Ser	Met	Thr	Cys	Glu	Lys	Phe	Phe	Ser	Gly	Gly	Cys	His	Arg	Asn	Arg	100	105	110	
	Ile	Glu	Asn	Arg	Phe	Pro	Asp	Glu	Ala	Thr	Cys	Met	Gly	Phe	Cys	Ala	115	120	125	
25	Pro	Lys	Lys	Ile	Pro	Ser	Phe	Cys	Tyr	Ser	Pro	Lys	Asp	Glu	Gly	Leu	130	135	140	
30	Cys	Ser	Ala	Asn	Val	Thr	Arg	Tyr	Tyr	Phe	Asn	Pro	Arg	Tyr	Arg	Thr	145	150	155	160
	Cys	Asp	Ala	Phe	Thr	Tyr	Thr	Gly	Cys	Gly	Gly	Asn	Asp	Asn	Asn	.Phe	165	170	175	
35	Val	Ser	Arg	Glu	Asp	Cys	Lys	Arg	Ala	Cys	Ala	Lys	Ala	Leu	Lys	Lys	180	185	190	
40	Lys	Lys	Lys	Met	Pro	Lys	Leu	Arg	Phe	Ala	Ser	Arg	Ile	Arg	Lys	Ile	195	200	205	
	Arg	Lys	Lys	Gln	Phe												210			
45																				